

Sequencing, Finishing, and Analysis in the Future (SFAF)

La Fonda on the Plaza, Santa Fe, NM — May 29th – May 31st, 2013

Call for Abstracts (both talks and posters) Deadline April 8th, 2013

Please join us for the 8th annual "Sequencing, Finishing and Analysis in the Future" Meeting on Wednesday, **May 29th through May 31st** in beautiful, historic Santa Fe, New Mexico. The three day SFAF conference will focus on Next Generation Sequencing technologies, applications, and their effect on the rapidly advancing field of Genomics.

Keynote Speakers:

- Richard Gibbs, Ph.D., Director, Human Genome Sequencing Center, Baylor College of Medicine (BCM)
- Mark Adams, Ph.D., Scientific Director, J. Craig Venter Institute (JCVI)
- Deanna Church, Ph.D., Staff Scientist & Coordinator of Variation Resources at NCBI

Areas to be emphasized include, but are not limited to the following:

Genome Sequencing:

- Sequencing technology advancements (454, illumina, Ion, MiSeq, PacBio, etc.)
- Draft sequencing strategies (prokaryotes, eukaryotes, metagenomics, single cell, etc.)
- *De novo* sequencing, re-sequencing, Human seq., RNA seq., metagenomics, etc.
- Sequencing applications for Metagenomics, Forensics, and Biosurveillance

Genome Assembly:

- Whole genome assemblers and integration of next generation data
- *De novo* assemblers for short reads, hybrid assemblers
- Recalling and calibrating genome assemblies
- Single cell and metagenomic assemblies

Genome Finishing / Improvement:

- Next Generation Finishing tools, technologies, and pipelines
- Human Genomics and genome improvement
- Quality standards for new technologies and mixed data sets
- Single cell / cell sorting and metagenomic finishing

Genome Analysis:

- Genome annotation and pathway identification tools and pipelines
- Comparative genomics, re-sequencing, SNPs, structural variation
- Large scale data management, cloud computing
- Analysis applications for Forensics, Metagenomics, and Biosurveillance



The conference is being sponsored by numerous genomics/sequencing vendors and hosted by the Los Alamos National Laboratory, thus **NO** registration fee is required. Participants need to cover travel costs, hotel and dinner charges. Breakfast, lunch and snacks will be provided. A block of rooms (**SFAF**) are reserved at the La Fonda at a special conference rate of \$83 per night. **A limited number of extra rooms are available the weekend before & after the conference for those that want to stay in the area a little longer (contact Chris Detter for more info).**

Registration is limited to 200; please register soon if you plan to attend. **To register, submit an abstract, or obtain more information as it becomes available please visit our web site, <http://www.lanl.gov/finishinginthefuture/>. Registration will follow the same guidelines as in 2012 (see website for meeting information updates).**

If you have any questions, or would like further information, please contact Chris Detter at (505)667-1326 or cdetter@lanl.gov.

We look forward to seeing you there!!!

The 2013 "Sequencing, Finishing and Analysis in the Future" Organizing Committee:

- * Chris Detter, Ph.D., BioThreat / BioDefense Program Director, LANL
- * Johar Ali, Ph.D., Cancer Genomics Team Leader, OICR
- * Patrick Chain, Bioinformatics/Metagenomics Team Leader, LANL
- * Michael FitzGerald, Microbial Special Projects Manager, Broad Institute
- * Bob Fulton, M.S., Director of Project Development & Management, WashU
- * Darren Grafham, Lab Manager, Children's Hospital, Sheffield, UK
- * Alla Lapidus, Ph.D., Associate Director, Algorithmic Biology Lab, SPbSU, Russia
- * Donna Muzny, M.Sc., Director of Operations, BCM
- * Nadia Fedorova, Genome Finishing and Analysis Team Leader, JCVI

